

SEQUENCE LISTING

SEQ ID NO: 1

SEQUENCE LENGTH: 21

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

SEQUENCE DESCRIPTION:

CTC TAG CAT GCG AAA ATC TAG

SEQ ID NO: 2

SEQUENCE LENGTH: 20

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

SEQUENCE DESCRIPTION:

CTG CAG GCC TGC AAG CTT GG

SEQ ID NO: 3

SEQUENCE LENGTH: 23

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

SEQUENCE DESCRIPTION:

ATC CTT TGT ATT TGA TTA AAG

SEQ ID NO: 4

SEQUENCE LENGTH: 20

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid

SEQUENCE DESCRIPTION:

TCT AGA GTC GAC CTG CAG GC

SEQ ID NO: 5

SEQUENCE LENGTH: 552

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE: Luciola cruciata and Photinus pyralis

SEQUENCE DESCRIPTION:

Met	Glu	Asn	Met	Glu	Asn	Asp	Glu	Asn	Ile	Val	Val	Gly	Pro	Lys	
1				5						10					15
Pro	Phe	Tyr	Pro	Ile	Glu	Glu	Gly	Ser	Ala	Gly	Thr	Gln	Leu	Arg	
				20						25					30
Lys	Tyr	Met	Glu	Arg	Tyr	Ala	Lys	Leu	Gly	Ala	Ile	Ala	Phe	Thr	
				35					40					45	
Asn	Ala	Val	Thr	Gly	Val	Asp	Tyr	Ser	Tyr	Ala	Glu	Tyr	Leu	Glu	
				50					55					60	
Lys	Ser	Cys	Cys	Leu	Gly	Lys	Ala	Leu	Gln	Asn	Tyr	Gly	Leu	Val	
				65					70					75	
Val	Asp	Gly	Arg	Ile	Ala	Leu	Cys	Ser	Glu	Asn	Cys	Glu	Glu	Phe	
				80					85					90	
Phe	Ile	Pro	Val	Ile	Ala	Gly	Leu	Phe	Ile	Gly	Val	Gly	Val	Ala	
				95					100					105	
Pro	Thr	Asn	Glu	Ile	Tyr	Thr	Leu	Arg	Glu	Leu	Val	His	Ser	Leu	
				110					115					120	
Gly	Ile	Ser	Lys	Pro	Thr	Ile	Val	Phe	Ser	Ser	Lys	Lys	Gly	Leu	
				125					130					135	
Asp	Lys	Val	Ile	Thr	Val	Gln	Lys	Thr	Val	Thr	Thr	Ile	Lys	Thr	
				140					145					150	
Ile	Val	Ile	Leu	Asp	Ser	Lys	Val	Asp	Tyr	Arg	Gly	Tyr	Gln	Cys	
				155					160					165	
Leu	Asp	Thr	Phe	Ile	Lys	Arg	Asn	Thr	Pro	Pro	Gly	Phe	Gln	Ala	
				170					175					180	
Ser	Ser	Phe	Lys	Thr	Val	Glu	Val	Asp	Arg	Lys	Glu	Gln	Val	Ala	

Leu	Ile	Met	Asn	185	Ser	Ser	Gly	Ser	Thr	Gly	Leu	Pro	Lys	Gly	Val
				200						205					210
Gln	Leu	Thr	His	215	Glu	Asn	Thr	Val	Thr	Arg	Phe	Ser	His	Ala	Arg
				230						220					225
Asp	Pro	Ile	Phe	235	Gly	Asn	Gln	Ile	Ile	Pro	Asp	Thr	Ala	Ile	Leu
				250						235					240
Ser	Val	Val	Pro	255	Phe	His	His	Gly	Phe	Gly	Met	Phe	Thr	Thr	Leu
				270						250					255
Gly	Tyr	Leu	Ile	275	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	Tyr	Arg	Phe
				290						265					270
Glu	Glu	Glu	Leu	295	Phe	Leu	Arg	Ser	Leu	Gln	Asp	Tyr	Lys	Ile	Gln
				310						280					285
Ser	Ala	Leu	Leu	315	Val	Pro	Thr	Leu	Phe	Ser	Phe	Phe	Ala	Lys	Ser
				330						295					300
Thr	Leu	Ile	Asp	335	Lys	Tyr	Asp	Leu	Ser	Asn	Leu	His	Glu	Ile	Ala
				350						310					315
Ser	Gly	Gly	Ala	355	Pro	Leu	Ser	Lys	Glu	Val	Gly	Glu	Ala	Val	Ala
				370						325					330
Lys	Arg	Phe	His	375	Leu	Pro	Gly	Ile	Arg	Gln	Gly	Tyr	Gly	Leu	Thr
				390						340					345
Glu	Thr	Thr	Ser	395	Ala	Ile	Leu	Ile	Thr	Pro	Glu	Gly	Asp	Asp	Lys
				410						355					360
Pro	Gly	Ala	Val	415	Gly	Lys	Val	Val	Pro	Phe	Phe	Glu	Ala	Lys	Val
				430						370					375
Val	Asp	Leu	Asp	435	Thr	Gly	Lys	Thr	Leu	Gly	Val	Asn	Gln	Arg	Gly
				450						385					390
Glu	Leu	Cys	Val	455	Arg	Gly	Pro	Met	Ile	Met	Ser	Gly	Tyr	Val	Asn
				470						400					405
Asn	Pro	Glu	Ala	475	Asn	Asn	Ala	Leu	Ile	Asp	Lys	Asp	Gly	Trp	Leu
				490						415					420
His	Ser	Gly	Asp	495	Ile	Ala	Tyr	Trp	Asp	Glu	Asp	Glu	His	Phe	Phe
				510						430					435
Ile	Val	Asp	Arg	525	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly	Tyr	Gln
				540						445					450
Val	Ala	Pro	Ala	545	Glu	Leu	Glu	Ser	Ile	Leu	Leu	Gln	His	Pro	Asn
				560						460					465
Ile	Phe	Asp	Ala	575	Gly	Val	Ala	Gly	Leu	Pro	Asp	Asp	Asp	Ala	Gly
				590						475					480
Glu	Leu	Pro	Ala	595	Ala	Val	Val	Val	Leu	Glu	His	Gly	Lys	Thr	Met
				610						490					495
Thr	Glu	Lys	Glu	615	Ile	Val	Asp	Tyr	Val	Ala	Ser	Gln	Val	Thr	Thr
				630						505					510
Ala	Lys	Lys	Leu	635	Arg	Gly	Gly	Val	Val	Phe	Val	Asp	Glu	Val	Pro
				650						520					525
Lys	Gly	Leu	Thr	655	Gly	Lys	Leu	Asp	Ala	Arg	Lys	Ile	Arg	Glu	Ile
				670						535					540
Leu	Ile	Lys	Ala	675	Lys	Lys	Gly	Gly	Lys	Ser	Lys	Lys	Leu		
				690						550					

SEQ ID NO: 6

SEQUENCE LENGTH: 1656

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE: Luciola cruciata and Photinus pyralis

SEQUENCE DESCRIPTION:

ATG	GAA	AAC	ATG	GAA	AAC	GAT	GAA	AAT	ATT	GTA	GTT	GGA	CCT	AAA	CCG	48
TTT	TAC	CCT	ATC	GAA	GAG	GGA	TCT	GCT	GGA	ACA	CAA	TTA	CGC	AAA	TAC	96
ATG	GAG	CGA	TAT	GCA	AAA	CTT	GGC	GCA	ATT	GCT	TTT	ACA	AAT	GCA	GTT	144
ACT	GGT	GTT	GAT	TAT	TCT	TAC	GCC	GAA	TAC	TTG	GAG	AAA	TCA	TGT	TGT	192
CTA	GGA	AAA	GCT	TTG	CAA	AAT	TAT	GGT	TTG	GTT	GTT	GAT	GGC	AGA	ATT	240
GCG	TTA	TGC	AGT	GAA	AAC	TGT	GAA	GAA	TTT	TTT	ATT	CCT	GTA	ATA	GCC	288
GGA	CTG	TTT	ATA	GGT	GTA	GGT	GTT	GCA	CCC	ACT	AAT	GAG	ATT	TAC	ACT	336
TTA	CGT	GAA	CTG	GTT	CAC	AGT	TTA	GGT	ATC	TCT	AAA	CCA	ACA	ATT	GTA	384
TTT	AGT	TCT	AAA	AAA	GGC	TTA	GAT	AAA	GTT	ATA	ACA	GTA	CAG	AAA	ACA	432
GTA	ACT	ACT	ATT	AAA	ACC	ATT	GTT	ATA	CTA	GAT	AGC	AAA	GTT	GAT	TAT	480
CGA	GGA	TAT	CAA	TGT	CTG	GAC	ACC	TTT	ATA	AAA	AGA	AAC	ACT	CCA	CCA	528
GGT	TTT	CAA	GCA	TCC	AGT	TTC	AAA	ACT	GTC	GAA	GTT	GAC	CGT	AAA	GAA	576
CAA	GTT	GCT	CTT	ATA	ATG	AAC	TCT	TCG	GGT	TCT	ACC	GGT	TTG	CCA	AAA	624
GGC	GTA	CAA	CTT	ACT	CAC	GAA	AAT	ACA	GTC	ACT	AGA	TTT	TCG	CAT	GCC	672
AGA	GAT	CCT	ATT	TTT	GGC	AAT	CAA	ATC	ATT	CCG	GAT	ACT	GCG	ATT	TTA	720
AGT	GTT	GTT	CCA	TTC	CAT	CAC	GGT	TTT	GGA	ATG	TTT	ACT	ACA	CTC	GGA	768
TAT	TTG	ATA	TGT	GGA	TTT	CGA	GTC	GTC	TTA	ATG	TAT	AGA	TTT	GAA	GAA	816
GAG	CTG	TTT	TTA	CGA	TCC	CTT	CAG	GAT	TAC	AAA	ATT	CAA	AGT	GCG	TTG	864
CTA	GTA	CCA	ACC	CTA	TTT	TCA	TTC	TTC	GCC	AAA	AGC	ACT	CTG	ATT	GAC	912
AAA	TAC	GAT	TTA	TCT	AAT	TTA	CAC	GAA	ATT	GCT	TCT	GGG	GGC	GCA	CCT	960
CTT	TCG	AAA	GAA	GTC	GGG	GAA	GCG	GTT	GCA	AAA	CGC	TTC	CAT	CTT	CCA	1008
GGG	ATA	CGA	CAA	GGG	TAT	GGG	CTC	ACT	GAG	ACT	ACA	TCA	GCT	ATT	CTG	1056
ATT	ACA	CCC	GAG	GGG	GAT	GAT	AAA	CCG	GGC	GGC	GTC	GGT	AAA	GTT	GTT	1104
CCA	TTT	TTT	GAA	GCG	AAG	GTT	GTC	GAT	CTG	GAT	ACC	GGG	AAA	ACG	CTG	1152
GGC	GTT	AAT	CAG	AGA	GGC	GAA	TTA	TGT	GTC	AGA	GGA	CCT	ATG	ATT	ATG	1200
TCC	GGT	TAT	GTA	AAC	AAT	CCG	GAA	GCG	ACC	AAC	GCC	TTG	ATT	GAC	AAG	1248
GAT	CGA	TGG	CTA	CAT	TCT	GGA	GAC	ATA	GCT	TAC	TGG	GAC	GAA	GAC	GAA	1296
CAC	TTC	TTC	ATA	GTT	GAC	CGC	TTG	AAG	TCT	TTA	ATT	AAA	TAC	AAA	GGA	1344
TAT	CAG	GTG	GCC	CCC	GCT	GAA	TTG	GAA	TCG	ATA	TTG	TTA	CAA	CAC	CCC	1392
AAC	ATC	TTC	GAC	GCG	GGC	GTG	GCA	GGT	CTT	CCC	GAC	GAT	GAC	GCC	GGT	1440
GAA	CTT	CCC	GCC	GCC	GTT	GTT	GTT	TTG	GAG	CAC	GGA	AAG	ACG	ATG	ACG	1488
GAA	AAA	GAG	ATC	GTG	GAT	TAC	GTC	GCC	AGT	CAA	GTA	ACA	ACC	GCG	AAA	1536
AAG	TTG	CGC	GGG	GGG	GTT	GTG	TTT	GTG	GAC	GAA	GTA	CCG	AAA	GGT	CTT	1584
ACC	GGA	AAA	CTC	GAC	GCA	AGA	AAA	ATC	AGA	GAG	ATC	CTC	ATA	AAG	GCC	1632
AAG	AAG	GGC	GGG	AAG	TCC	AAA	TTG									1656

SEQ ID NO: 7

SEQUENCE LENGTH: 552

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE: Luciola cruciata and Photinus pyralis

SEQUENCE DESCRIPTION:

Met	Glu	Asn	Met	Glu	Asn	Asp	Glu	Asn	Ile	Val	Val	Gly	Pro	Lys
1	5							10					15	
Pro	Phe	Tyr	Pro	Ile	Glu	Glu	Gly	Ser	Ala	Gly	Thr	Gln	Leu	Arg
	20								25				30	
Lys	Tyr	Met	Glu	Arg	Tyr	Ala	Lys	Leu	Gly	Ala	Ile	Ala	Phe	Thr
	35								40				45	
Asn	Ala	Val	Thr	Gly	Val	Asp	Tyr	Ser	Tyr	Ala	Glu	Tyr	Leu	Glu
	50								55				60	
Lys	Ser	Cys	Cys	Leu	Gly	Lys	Ala	Leu	Gln	Asn	Tyr	Gly	Leu	Val
	65								70				75	
Val	Asp	Gly	Arg	Ile	Ala	Leu	Cys	Ser	Glu	Asn	Cys	Glu	Glu	Phe
	80								85				90	
Phe	Ile	Pro	Val	Ile	Ala	Gly	Leu	Phe	Ile	Gly	Val	Gly	Val	Ala
	95								100				105	
Pro	Thr	Asn	Glu	Ile	Tyr	Thr	Leu	Arg	Glu	Leu	Val	His	Ser	Leu
	110								115				120	
Gly	Ile	Ser	Lys	Pro	Thr	Ile	Val	Phe	Ser	Ser	Lys	Lys	Gly	Leu
	125								130				135	
Asp	Lys	Val	Ile	Thr	Val	Gln	Lys	Thr	Val	Thr	Thr	Ile	Lys	Thr
	140								145				150	
Ile	Val	Ile	Leu	Asp	Ser	Lys	Val	Asp	Tyr	Arg	Gly	Tyr	Gln	Cys
	155								160				165	
Leu	Asp	Thr	Phe	Ile	Lys	Arg	Asn	Thr	Pro	Pro	Gly	Phe	Gln	Ala
	170								175				180	
Ser	Ser	Phe	Lys	Thr	Val	Glu	Val	Asp	Arg	Lys	Glu	Gln	Val	Ala
	185								190				195	
Leu	Ile	Met	Asn	Ser	Ser	Gly	Ser	Thr	Gly	Leu	Pro	Lys	Gly	Val
	200								205				210	
Gln	Leu	Thr	His	Glu	Asn	Ile	Val	Thr	Arg	Phe	Ser	His	Ala	Arg
	215								220				225	
Asp	Pro	Ile	Tyr	Gly	Asn	Gln	Val	Ser	Pro	Gly	Thr	Ala	Val	Leu
	230								235				240	
Thr	Val	Val	Pro	Phe	His	His	Gly	Phe	Gly	Met	Phe	Thr	Thr	Leu
	245								250				255	
Gly	Tyr	Leu	Ile	Cys	Gly	Phe	Arg	Val	Val	Met	Leu	Thr	Lys	Phe
	260								265				270	
Asp	Glu	Glu	Thr	Phe	Leu	Lys	Thr	Leu	Gln	Asp	Tyr	Lys	Cys	Thr
	275								280				285	
Ser	Val	Ile	Leu	Val	Pro	Thr	Leu	Phe	Ala	Ile	Leu	Asn	Lys	Ser
	290								295				300	
Glu	Leu	Leu	Asn	Lys	Tyr	Asp	Leu	Ser	Asn	Leu	Val	Glu	Ile	Ala
	305								310				315	
Ser	Gly	Gly	Ala	Pro	Leu	Ser	Lys	Glu	Val	Gly	Glu	Ala	Val	Ala
	320								325				330	
Arg	Arg	Phe	Asn	Leu	Pro	Gly	Val	Arg	Gln	Gly	Tyr	Gly	Leu	Thr
	335								340				345	
Glu	Thr	Thr	Ser	Ala	Ile	Ile	Ile	Thr	Pro	Glu	Gly	Asp	Asp	Lys
	350								355				360	

Pro	Gly	Ala	Ser	Gly	Lys	Val	Val	Pro	Leu	Phe	Lys	Ala	Lys	Val
				365					370					375
Ile	Asp	Leu	Asp	Thr	Lys	Lys	Ser	Leu	Gly	Pro	Asn	Arg	Arg	Gly
				380					385					390
Glu	Val	Cys	Val	Lys	Gly	Pro	Met	Leu	Met	Lys	Gly	Tyr	Val	Asn
				395					400					405
Asn	Pro	Glu	Ala	Thr	Lys	Glu	Leu	Ile	Asp	Glu	Glu	Gly	Trp	Leu
				410					415					420
His	Thr	Gly	Asp	Ile	Gly	Tyr	Tyr	Asp	Glu	Glu	Lys	His	Phe	Phe
				425					430					435
Ile	Val	Asp	Arg	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly	Tyr	Gln
				440					445					450
Val	Ala	Pro	Ala	Glu	Leu	Glu	Ser	Ile	Leu	Leu	Gln	His	Pro	Asn
				455					460					465
Ile	Phe	Asp	Ala	Gly	Val	Ala	Gly	Leu	Pro	Asp	Asp	Asp	Ala	Gly
				470					475					480
Glu	Leu	Pro	Ala	Ala	Val	Val	Val	Leu	Glu	His	Gly	Lys	Thr	Met
				485					490					495
Thr	Glu	Lys	Glu	Ile	Val	Asp	Tyr	Val	Ala	Ser	Gln	Val	Thr	Thr
				500					505					510
Ala	Lys	Lys	Leu	Arg	Gly	Gly	Val	Val	Phe	Val	Asp	Glu	Val	Pro
				515					520					525
Lys	Gly	Leu	Thr	Gly	Lys	Leu	Asp	Ala	Arg	Lys	Ile	Arg	Glu	Ile
				530					535					540
Leu	Ile	Lys	Ala	Lys	Lys	Gly	Gly	Lys	Ser	Lys	Lys	Leu		
				545					550				552	

SEQ ID NO: 8

SEQUENCE LENGTH: 1656

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE: Luciola cruciata and Photinus pyralis

SEQUENCE DESCRIPTION:

ATG	GAA	AAC	ATG	GAA	AAC	GAT	GAA	AAT	ATT	GTA	GTT	GGA	CCT	AAA	CCG	48
TTT	TAC	CCT	ATC	GAA	GAG	GGA	TCT	GCT	GGA	ACA	CAA	TTA	CGC	AAA	TAC	96
ATG	GAG	CGA	TAT	GCA	AAA	CTT	GGC	GCA	ATT	GCT	TTT	ACA	AAT	GCA	GTT	144
ACT	GGT	GTT	GAT	TAT	TCT	TAC	GCC	GAA	TAC	TTG	GAG	AAA	TCA	TGT	TGT	192
CTA	GGA	AAA	GCT	TTG	CAA	AAT	TAT	GGT	TTG	GTT	GAT	GGC	AGA	ATT	240	
GCG	TTA	TGC	AGT	GAA	AAC	TGT	GAA	GAA	TTT	TTT	ATT	CCT	GTA	ATA	GCC	288
GGA	CTG	TTT	ATA	GGT	GTA	GGT	GTT	GCA	CCC	ACT	AAT	GAG	ATT	TAC	ACT	336
TTA	CGT	GAA	CTG	GTT	CAC	AGT	TTA	GGT	ATC	TCT	AAA	CCA	ACA	ATT	GTA	384
TTT	AGT	TCT	AAA	AAA	GGC	TTA	GAT	AAA	GTT	ATA	ACA	GTA	CAG	AAA	ACA	432
GTA	ACT	ACT	ATT	AAA	ACC	ATT	GTT	ATA	CTA	GAT	AGC	AAA	GTT	GAT	TAT	480
CGA	GGA	TAT	CAA	TGT	CTG	GAC	ACC	TTT	ATA	AAA	AGA	AAC	ACT	CCA	CCA	528

GGT	TTT	CAA	GCA	TCC	AGT	TTC	AAA	ACT	GTG	GAA	GTT	GAC	CGT	AAA	GAA	576
CAA	GTT	GCT	CTT	ATA	ATG	AAC	TCT	TCG	GGT	TCT	ACC	GGT	TTG	CCA	AAA	624
GGC	GTA	CAA	CTT	ACT	CAC	GAA	AAT	ACA	GTC	ACT	AGA	TTT	TCT	CAT	GCT	672
AGA	GAT	CCG	ATT	TAT	GGT	AAC	CAA	GTT	TCA	CCA	GGC	ACC	GCT	GTT	TTA	720
ACT	GTC	GTT	CCA	TTC	CAT	CAT	GGT	TTT	GGT	ATG	TTC	ACT	ACT	CTA	GGG	768
TAT	TTA	ATT	TGT	GGT	TTT	CGT	GTT	GTA	ATG	TTA	ACA	AAA	TTC	GAT	GAA	816
GAA	ACA	TTT	TTA	AAA	ACT	CTA	CAA	GAT	TAT	AAA	TGT	ACA	AGT	GTT	ATT	864
CTT	GTA	CCG	ACC	TTG	TTT	GCA	ATT	CTC	AAC	AAA	AGT	GAA	TTA	CTC	AAT	912
AAA	TAC	GAT	TTG	TCA	AAT	TTA	GTT	GAG	ATT	GCA	TCT	GGC	GGA	GCA	CCT	960
TTA	TCA	AAA	GAA	GTT	GGT	GAA	GCT	GTT	GCT	AGA	CGC	TTT	AAT	CTT	CCC	1008
GGT	GTT	CGT	CAA	GGT	TAT	GGT	TTA	ACA	GAA	ACA	ACA	TCT	GCC	ATT	ATT	1056
ATT	ACA	CCG	GAA	GGT	GAC	GAT	AAA	CCA	GGA	GCT	TCT	GGA	AAA	GTC	GTG	1104
CCG	TTG	TTT	AAA	GCA	AAA	GTT	ATT	GAT	CTT	GAT	ACC	AAA	AAA	TCT	TTA	1152
GGT	CCT	AAC	AGA	CGT	GGA	GAA	GTT	TGT	GTT	AAA	GGA	CCT	ATG	CTT	ATG	1200
AAA	GGT	TAT	GTA	AAT	AAT	CCA	GAA	GCA	ACA	AAA	GAA	CTT	ATT	GAC	GAA	1248
GAA	GGT	TGG	CTG	CAC	ACC	GGA	GAT	ATT	GGA	TAT	TAT	GAT	GAA	GAA	AAA	1296
CAT	TTC	TTT	ATT	GTC	GAT	CGT	TTG	AAG	TCT	TTA	ATC	AAA	TAC	AAA	GGA	1344
TAT	CAG	GTG	GCC	CCC	GCT	GAA	TTG	GAA	TCG	ATA	TTG	TTA	CAA	CAC	CCC	1392
AAC	ATC	TTC	GAC	GCG	GGC	GTG	GCA	GGT	CTT	CCC	GAC	GAT	GAC	GCC	GGT	1440
GAA	CTT	CCC	GCC	GCC	GTT	GTT	GTT	TTG	GAG	CAC	GGA	AAG	ACG	ATG	ACG	1488
GAA	AAA	GAG	ATC	GTG	GAT	TAC	GTC	GCC	AGT	CAA	GTA	ACA	ACC	GCG	AAA	1536
AAG	TTG	CGC	GGA	GGA	GTT	GTG	TTT	GTG	GAC	GAA	GTA	CCG	AAA	GGT	CTT	1584
ACC	GGG	AAA	CTC	GAC	GCA	AGA	AAA	ATC	AGA	GAG	ATC	CTC	ATA	AAG	GCC	1632
AAG	AAG	GGC	GGA	AAG	TCC	AAA	TTG									1656